

Structure of LCP1 and alignments of domains

FIG. 1A



FIG. 1B

CUB domain		10	20	30	40	50	60	70	80
consensus	********
LCP1	1	CGGTLTAS-S-	GTITSPNPN	SYNNINLCV	WTISAPPGY-	RIELKFTDF-	DLESSD-	NCTYDYVEI	YDGPSTSSP
1SP_B	26	CGHTVLGPes-	GTILTSINYP	QTYPNSTVC	WEIEIRVKME-	RVRIKFGDF-	DIEDSD-	SCHFNYLRI	YNGIGVSR
gi 1345609	9	CGRVIKDT-S-	GSISNDRÖK-	NLCTWTIIM	KPDÖ-KVMAIPY-	LNLA-		CGKEYVEV	FDGLL-SGP
gi 1168684	752	CEHKVTSTs-	GTITSPNWP	DKYPSKKECT	WAISSTPGH-	RVKLTfVEm-	DIESqp-	eCAYDHL	EVFDGRDAKAP
gi 5912464	484	CGGSFGGTq--	GRVATPNYP	NnyndleCV	VVIEVEIGR-	RVELDFIDf-	VLEDet-	ncRWDsL	SINLGDG--IK
gi 2498677	1766	CGGFLFYA-S-	GTFSSPSYP	AYYPNAKVC	WEIEVNSGY-	RINLGSN1-	KLEAh-	ncSFDY	VEIFDGSlnSSL
gi 2055303	25	CGDTIKIL-Sp-	GYLTSPGYP	ÖsyhpsÖKCE	WLIOAPEPYq	RIMINFNPh	fDLEdr-	dCKYD	VEVIDGDNaEGR
gi 1899042	17	vfSAELLT-Ahf	GNFSSPNY	PRsyPdsn	SLTNIRVÖHGy-	RMSIRfst-	fDLEDsyed	gigsCVYD	VEITESN---K
gi 704441	520	CGGNMPGP-E-	GFLNSPAY	PDeysdkVC	CEWVITVREGY-	QVAlEFATf-	ETEFdp-	dCAYDY	VEIRDGDTKDS
	3	CGHTVLGP-Es-	GTILTSINYP	ÖltpnstVC	WEIEIRVKME-	RVRIKFGDf-	DIEDsd-	SCHFNYLRI	YNGIGVSR

	90	100	110	120	130
consensus*.....*.....*.....*.....				
LCP1	71 LIGRFGG-SEL-----PPPISSSSNSMTVTfVSDSSVÖKRGFsARYSAV	97 EIGKYCGIGLÖ-----MNSIESKGNETILLfMSGIHVSGRGFLASYSVI	69 SYGKLCA-GA-----AIVFLSTA-NTMTIKYNRISGNSSSPFLIYFYGs	822 VLGRFGG-SKk-----PEPVLATg-NRMFLRFYSDNSVÖRKGFÖASHSTE	552 IDMKMCG-REY-----PAASLVSIGNNMELTILISDRSVtdRGFMADYRAI
1SP_B	gi 1345609	822 VLGRFGG-SKk-----PEPVLATg-NRMFLRFYSDNSVÖRKGFÖASHSTE	552 IDMKMCG-REY-----PAASLVSIGNNMELTILISDRSVtdRGFMADYRAI	595	
gi 1168684	552 IDMKMCG-REY-----PAASLVSIGNNMELTILISDRSVtdRGFMADYRAI	595			
gi 5912464	1836 LIGKICN-DT-----RÖIFTSSYNRMTHFRSDISfÖNTGFLAWYNSf	1877			
gi 2498677	97 LMGRYCG-KIA-----PPPLVSSg-PYLfIKfVSDYETHGAGFSIRYEVf	139			
gi 2055303	90 TVAKRFGG-NYqlfptdapnPSKfIYTSqNEVRVTfVSDYSISLSGfÖAHYAÖI	141			
gi 1899042	590 LVGTfYCG-TRt-----PPNAISTs-RHLVYKfVSDESMÖKGGSASYLEE	632			
gi 704441	74 EIGKYCG-LG1-----qINHSIESKGNETILLfMSGIHVSGRGFLASYSVI	118			

FIG. 1C
LCCL domain

		10	20	30	40	50	60	70	80
consensus	1	QAVTCDTKALDLC	--KPVTD	CNRVHCPAGCLLPK	--AKVFGTL	--VYASLSSICRAVHAGVIDNTSGGAVDVVRVGG	72		
LCPI	145	dLITCLDTASNFL	--EPEFSK	--YCPAGCLLPF	--AEISGTI	phGYRDSPLCMAGVHAGVVSNTLGGQTSVVISKG	215		
gi 12053227	387	QDLDCYTTVAQLCP	feKPATHCPRIHCPAHCKDEP	sywAPVFGTN	--IYADTSSIC	KTAVHAGVISNESGGDVDPVVDK	464		
gi 12002311	291	QIVSCEVRLRDQC	--KGTT	CNRYECPAGCLDSK	--AKVIGSV	--HYEMQSSICRAAIHYGIIDND	--GGVVDITRQGR	360	
gi 12002311	392	QAVTCETTVEQLCP	fhKPASHCPRVYCPRNCMQANph	YARVIGTR	--VYSDLSSICRAVHAGVVRNH	--GGYVDVMPVDK	468		
gi 12053227	286	QVVRCDTKMKDRC	--KGST	CNRYQCPAGCLNHK	--AKIFGTL	--FYESSSSICRAAIHYGIIDDK	--GGLVDITRNGK	355	
gi 7387581	26	NAITCFTTRGLDLR	--KETED	--VLCRANCPLMQ	--FYVEGDG	--IYASLSSVCGAAIHRGVITN	--AGGAVRVQTLPG	93	
gi 12644458	32	IPVTCFTTRGLDIR	--KEKAD	--VLCRPGGCSLEE	--FSVFGNI	--VYASVSSICGAAVHRGVIGT	--SGGPVRVYSLPG	99	
gi 7044441	126	LFGHCIQFFWNLS	--SVST	--APAGCLLPF	--AEISGTI	phGYRDSPLCMAGVHAGVVSNTLGGQTSVVISKG	193		
gi 913964	391	REVDCDSKAVDFL	--DDVGE	PVRIHCPAGCSLTA	--GTVMGTA	--IYHELSSVCRAAIHAGKLPN	--SGGAVHVVANNGP	461	
gi 6624095	42	PQINCDVKAGKII	--DPEFI	--VKCPAGCQDPK	--YHVGTD	--VYASYSVCGAAVHSGVLDN	--SGGKILVRKVAG	109	

		90
consensus	73	QPYIIGSLANGIQSE 87
LCPI	216	IPYESSLANNVTSV 230
gi 12053227	465	KKTYVGSIRNGVQSE 479
gi 12002311	361	KHYFIKSNRNGIQTI 375
gi 12002311	469	RKTYIASFQNGIFSE 483
gi 12053227	356	VPFFVKSERHGVQSL 370
gi 7387581	94	QENYPAVHANGIQSQ 108
gi 12644458	100	RENYSSVDANGIQSQ 114
gi 7044441	194	IPYESSLANNVTSV 208
gi 913964	462	YSDFLGSDLNGIKSE 476
gi 6624095	110	QSGYKGSYSNGVQSL 124

FIG. 1D **DSD/FA58C domain**

consensus	1	PLGMESG-RIPDSQITASSS----	YSAN-----	WTPENARLNSQGAGAMSPK----	ANDQNQWLQVDLGKPRRYT	62		
LCPI	249	tlgmESG-VIADPQITASSVlewt	htgQENS-----	wkPKARLKKPPD--	WAAF--	ATDEYQWLQIDLNKEKKIT	316	
LCZI_A	5	PLGMENG-KIENKQITASSF-----	KKSwg--	dyMEPRARLINAQGRVNAWQAK----	ANNNKQWL	EIDILKIKKIT	70	
LD7P_M	7	PLGMESK-AISDAQITASSY-----	FTNwf-----	twSPSKARLHLQGRSNARBPQ----	VNNPKEWLQVDFQKTMKYT	71		
gi 2547128	280	PLGMESG-RIANEQISASST-----	FSDgr-----	WTPQQRHLGDD--	NGWTPN----	LDNKEYLQVDLRFILMTL	340	
gi 2506380	233	PLGLKNN-SIPDKQITASSS-----	YKtwglhl	fswNPSYARLDQGNFNNAVAG----	SYGNDQWLQVDLGSSKEVT	300		
gi 127058	311	PLGLKNN-TIPDSQMSASSS-----	YKtwnl	rafgywYpHLGRLDNQGKINAWTAQ----	SNSAKEWLQVDLGTQRQVT	378		
gi 2645493	2035	PLGMASG-HIRDFQITASGQ-----	YGQ-----	WAPKLARLHYSGSINAWSTKd--	PFS--	WIKVDLAPMILH	2093	
gi 2623894	322	PLGMKSG-HIQDYQITASSV-----	FRTlmdmft	wEPKARLDQGNVNAWTSg--	HNDQSQWLQVDILVPTKYT	389		
gi 704441	228	TLGMESGgDRGSSNNSITVL-----	EWTdhtg	enswKP--	KKSQAEK--	twTAlga	fATDEYQWLQIDLNKEKKIT	295

consensus	63	GVITQGRKDFGSS--	QWTSYKQYSDDERTW	TYKGD--	GKPKIFP	GNSDRNT--	PVTNDFD	DP	IVAR	YIRILP	LTHG	137	
LCPI	317	GIITGSTMEHN--	YVSA	YRILYSDDGQKWT	YREPGEQDKIFQ	GNKDYHQ--	DYRNNFL	PLPILARF	IRVNP	QWQ	392		
LCZI_A	71	AIITQGCKSLSE--	MYVKS	YTIHYSEQVEMKPYRLKS	mwDKIFEGNT	NTKG--	HVKNFEN	DPILSRF	IRV	IPKTMQ	146		
LD7P_M	72	GVTTQGVKSLTS--	MYVKE	FLISSQDGHQWTLFFQN--	GKVKVFQ	GNQDSFT--	PVNVCLD	BPILLTRYLRI	HPQSWH	145			
gi 2547128	341	AIATQGAISRETQK--	gyVVKSYKLE	VSTNGEDW	MYRRHG--	KNHKIFQ	ANDDATE--	VYLNK	LHMPILLTRF	IRIPQTMHL	416		
gi 2506380	301	GIITQGARNFSGV--	QFVAS	YKVAYSNDSANWTEYQ	DPRTGSSKIF	PGNWDNHS--	HKKNL	FETPILAR	YRILPV	AWHN	376		
gi 127058	379	GIITQGARDFGHI--	QYVES	YKVAHSDDGQWTVYEEQ--	GSSKVFQ	GNLDNNS--	HKKNL	FEKPF	WAR	YRVLPV	SWHN	452	
gi 2645493	2094	GIITQGARQKFSS--	LYVSQ	FIIMYSLDGNK	WHSYRGNS	tGTLmVFF	GNVDSSG--	IKHN	IFNP	PIIAQYIRL	HPHYSI	2169	
gi 2623894	390	GIITQGA	KDFGHV--	QFVGSYK	LAYSNDGEH	MMVHQDEK	qRKDKVFQ	GNF	NDNT--	HRKNV	IDPPIYARF	IRILPWSWYG	465
gi 704441	296	GIITGST	MVSTltmclPTES	CTVMGRNGL--	CTES	lyve-QD--	KIFQGNK	RIIT	mVRNNFL	PLPILAR-----	361		

consensus	138	RI	139
LCPI	393	KI	394
LCZI_A	147	SI	148
LD7P_M	146	QI	147
gi 2547128	417	GI	418
gi 2506380	377	RI	378
gi 127058	453	RI	454
gi 2645493	2170	RS	2171
gi 2623894	466	RI	467
gi 704441	362	-L	362

FIG. 2

ut: SEQ ID NO: 1

aa: SEQ ID NO: 3

FIG. 3

[illegible]

FIG. 3

176	Y	C	P	A	G	C	L	L	P	F	A	E	I
603	TAC	TGC	CCA	GCT	GCT	TGT	CTG	CTT	CCT	TTT	GCT	GAG	ATA
189	S	G	T	I	P	H	G	Y	R	D	S	S	P
642	TCT	GGA	ACA	ATT	CCT	CAT	GGA	TAT	AGA	GAT	TCC	TCG	CCA
202	L	C	M	A	G	V	H	A	G	V	V	S	N
681	TTG	TGC	ATG	GCT	GCT	GTT	GCA	GGA	GTA	GTG	TCA	AAC	
215	T	L	G	G	G	Q	I	S	V	V	I	S	K
720	ACG	TTG	GGC	GGC	CAA	ATC	AGT	GTT	GTA	ATT	AGT	AAA	GGT
228	I	P	Y	Y	E	S	S	L	A	N	N	V	T
759	ATT	CCC	TAT	TAT	GAA	AGT	TCT	TTG	GCT	AAC	AAC	GTC	ACA
241	S	V	V	G	H	L	S	T	S	L	F	T	F
798	TCT	GTG	GTG	GGA	CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT
254	K	T	S	G	C	Y	G	T	L	G	M	E	S
837	AAG	ACA	AGT	GGA	TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT
267	G	V	I	A	D	P	Q	I	T	A	S	S	V
876	GGT	GTG	ATC	GCG	GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG
280	L	E	W	T	D	H	T	G	Q	E	N	S	M
915	CTG	GAG	TGG	ACT	GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG
293	K	P	K	K	A	R	L	K	K	P	G	P	P
954	AAA	CCC	AAA	AAA	GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT
306	W	A	A	F	A	T	D	E	Y	Q	W	L	Q
993	TGG	GCT	GCT	TTT	GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA
319	I	D	L	N	K	K	E	K	K	I	T	G	I
1032	ATA	GAT	TTG	AAT	AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA
332	T	T	G	S	T	M	V	E	H	N	Y	Y	V
1071	ACC	ACT	GGA	TCC	ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG
345	S	A	Y	R	I	L	Y	S	D	D	G	Q	K
1110	TCT	GCC	TAC	AGA	ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA
358	W	T	V	Y	R	E	P	G	V	E	Q	D	K
1149	TGG	ACT	GTG	TAC	AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG
371	I	F	Q	G	N	K	D	Y	H	Q	D	V	R
1188	ATA	TTT	CAA	GGA	AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT
384	N	N	F	L	P	P	I	I	A	R	F	I	R
1227	AAT	AAC	TTT	TTG	CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA

FIG. 3

397	V	N	P	T	Q	W	Q	Q	K	I	A	M	K
1266	GTG	AAT	CCT	ACC	CAA	TGG	CAG	CAG	AAA	ATT	GCC	ATG	AAA
410	M	E	L	L	G	C	Q	F	I	P	K	G	R
1305	ATG	GAG	CTG	CTC	GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT
423	P	P	K	L	T	Q	P	P	P	P	R	N	S
1344	CCT	CCA	AAA	CCT	ACT	CAA	CCT	CCA	CCT	CGG	AAC	AGC	
436	N	D	L	K	N	T	T	A	P	P	K	I	A
1383	AAT	GAC	CTC	AAA	AAC	ACT	ACA	GCC	CCT	CCA	AAA	ATA	GCC
449	K	G	R	A	P	K	F	T	Q	P	L	Q	P
1422	AAA	GGT	CGT	GCC	CCA	AAA	TTT	ACG	CAA	CCA	CTA	CAA	CCT
462	R	S	S	N	E	F	P	A	Q	T	E	Q	T
1461	CGC	AGT	AGC	AAT	GAA	TTT	CCT	GCA	CAG	ACA	GAA	CAA	ACA
475	T	A	S	P	D	I	R	N	T	T	V	T	P
1500	ACT	GCC	AGT	CCT	GAT	ATC	AGA	AAT	ACT	ACC	GTA	ACT	CCA
488	N	V	T	K	D	V	A	L	A	A	V	L	V
1539	AAT	GTA	ACC	AAA	GAT	GTA	GCG	CTG	GCT	GCA	GTT	CCT	GTC
501	P	V	L	V	M	V	L	T	T	L	I	L	I
1578	CCT	GTG	CTG	CTG	ATG	GTC	CTC	ACT	ACT	CTC	ATT	CTC	ATA
514	L	V	C	A	W	H	W	R	N	R	K	K	K
1617	TTA	GTG	TGT	GCT	TGG	CAC	TGG	AGA	AAC	AGA	AAA	AAA	AAA
527	T	E	G	T	Y	D	L	P	Y	W	D	R	A
1656	ACT	GAA	GGC	ACC	TAT	GAC	TTA	CCT	TAC	TGG	GAC	CGG	GCA
540	G	W	W	K	G	M	K	Q	F	L	P	A	K
1695	GGT	TGG	TGG	AAA	GGA	ATG	AAG	CAG	TTT	CTT	CCT	GCA	AAA
553	A	V	D	H	E	E	T	P	V	R	Y	S	S
1734	GCA	GTG	GAC	CAT	GAG	GAA	ACC	CCA	GTT	CGC	TAT	AGC	AGC
566	S	E	V	N	H	L	S	P	R	E	V	T	T
1773	AGC	GAA	GTT	AAT	CAC	CTG	AGT	CCA	AGA	GAA	GTC	ACC	ACA
579	V	L	Q	A	D	S	A	E	Y	A	Q	P	L
1812	GTG	CTG	CTG	CAG	GCT	GAC	TCT	GCA	GAG	TAT	GCT	CAG	CTG
592	V	G	G	I	V	G	T	L	H	Q	R	S	T
1851	GTA	GGA	GGA	GGA	ATT	GTT	GGT	ACA	CTT	CAT	CAA	AGA	TCT
605	F	K	P	E	E	G	K	E	A	G	Y	A	D
1890	TTT	AAA	CCA	GAA	GAA	GAA	AAA	GAA	GCA	GGC	TAT	GCA	GAC
618	L	D	P	Y	N	S	P	G	Q	E	V	Y	H
1929	CTA	GAT	CCT	TAC	AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT

FIG. 3

631	A	Y	A	E	P	L	P	I	T	G	P	E	Y
1968	GCC	TAT	GCT	GAA	CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT
644	A	T	P	I	I	M	D	M	S	G	H	P	T
2007	GCA	ACC	CCA	ATC	ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA
657	T	S	V	G	Q	P	S	T	S	T	F	K	A
2046	ACT	TCA	GTT	GGT	CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT
670	T	G	N	Q	P	P	P	L	V	G	T	Y	N
2085	ACG	GGG	AAC	CAA	CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT
683	T	L	L	S	R	T	D	S	C	S	S	A	Q
2124	ACA	CTT	CTC	TCC	AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG
696	A	Q	Y	D	T	P	K	A	G	K	P	G	L
2163	GCC	CAG	TAT	GAT	ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA
709	P	A	P	D	E	L	V	Y	Q	V	P	Q	S
2202	CCT	GCC	CCA	GAC	GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC
722	T	Q	E	V	S	G	A	G	R	D	G	E	C
2241	ACA	CAA	GAA	GTA	TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT
730	D	V	F	K	E	I	L	*	agatgctgctgctt				
2280	GAT	GTT	TTT	AAA	GAA	ATC	CTT	TGA					

[illegible]

FIG. 4

169	H	L	S	T	S	L	F	T	F	T	A	ACA	TTT	ACA	TTT	AAG	ACA	AGT	GGA
507	CAC	TTA	TCT	ACA	AGT	CTT	TTT	ACA	TTT	AAG	ACA	AGT	GGA						
182	C	Y	G	T	L	G	M	E	S	G	V	I	A						
546	TGT	TAT	GGA	ACA	CTG	GGG	ATG	GAG	TCT	GGT	GTG	ATC	GCG						
195	D	P	Q	I	T	A	S	S	V	L	E	W	T						
585	GAT	CCT	CAA	ATA	ACA	GCA	TCA	TCT	GTG	CTG	GAG	TGG	ACT						
208	D	H	T	G	Q	E	N	S	W	K	P	K	K						
624	GAC	CAC	ACA	GGG	CAA	GAG	AAC	AGT	TGG	AAA	CCC	AAA	AAA						
221	A	R	L	K	K	P	G	P	P	W	A	A	F						
663	GCC	AGG	CTG	AAA	AAA	CCT	GGA	CCG	CCT	TGG	GCT	GCT	TTT						
234	A	T	D	E	Y	Q	W	L	Q	I	D	L	N						
702	GCC	ACT	GAT	GAA	TAC	CAG	TGG	TTA	CAA	ATA	GAT	TTG	AAT						
247	K	E	K	K	I	T	G	I	I	T	T	G	S						
741	AAG	GAA	AAG	AAA	ATA	ACA	GGC	ATT	ATA	AAC	ACT	GGA	TCC						
260	T	M	V	E	H	N	Y	Y	V	S	A	Y	R						
780	ACC	ATG	GTG	GAG	CAC	AAT	TAC	TAT	GTG	TCT	GCC	TAC	AGA						
273	I	L	Y	S	D	D	G	Q	K	W	T	V	Y						
819	ATC	CTG	TAC	AGT	GAT	GAT	GGG	CAG	AAA	TGG	ACT	GTG	TAC						
286	R	E	P	G	V	E	Q	D	K	I	F	Q	G						
858	AGA	GAG	CCT	GGT	GTG	GAG	CAA	GAT	AAG	ATA	TTT	CAA	GGA						
299	N	K	D	Y	H	Q	D	V	R	N	N	F	L						
897	AAC	AAA	GAT	TAT	CAC	CAG	GAT	GTG	CGT	AAT	AAC	TTT	TTG						
312	P	P	I	I	A	R	F	I	R	V	N	P	T						
936	CCA	CCA	ATT	ATT	GCA	CGT	TTT	ATT	AGA	GTG	AAT	CCT	ACC						
325	Q	W	Q	Q	K	I	A	M	K	M	E	L	L						
975	CAA	TGG	CAG	CAG	AAA	ATT	GCC	ATG	AAA	ATG	GAG	CTG	CTC						
338	G	C	Q	F	I	P	K	G	R	P	P	K	L						
1014	GGA	TGT	CAG	TTT	ATT	CCT	AAA	GGT	CGT	CCT	CCA	AAA	CTT						

FIG. 4

533	E	G	K	E	A	G	Y	A	D	L	D	P	Y
1560	GTT	GGT	ACA	CTT	CAT	CAA	AGA	TCT	ACC	TTT	AAA	CCA	GAA
520	V	G	T	L	H	Q	R	S	T	F	K	P	E
1521	GAC	TCT	GCA	GAG	TAT	GCT	CAG	CCA	CTG	GTA	GGA	GGA	ATT
507	D	S	A	E	Y	A	Q	P	L	V	G	G	I
1482	CAC	CTG	AGT	CCA	AGA	GAA	GTC	ACC	ACA	GTG	CTG	CAG	GCT
494	H	L	S	P	R	E	V	T	T	V	L	Q	A
1443	GAG	GAA	ACC	CCA	GTT	CGC	TAT	AGC	AGC	AGC	GAA	GTT	AAT
481	E	E	T	P	V	R	Y	S	S	S	E	V	N
1404	GGA	ATG	AAG	CAG	TTT	CTT	CCT	GCA	AAA	GCA	GTG	GAC	CAT
468	G	M	K	Q	F	L	P	A	K	A	V	D	H
1365	TAT	GAC	TTA	CCT	TAC	TGG	GAC	CGG	GCA	GGT	TGG	TGG	AAA
455	Y	D	L	P	Y	W	D	R	A	G	W	W	K
1326	TGG	CAC	TGG	AGA	AAC	AGA	AAG	AAA	AAA	ACT	GAA	GGC	ACC
442	W	H	W	R	N	R	K	K	K	T	E	G	T
1287	ATG	GTC	CTC	ACT	ACT	CTC	ATT	CTC	ATA	TTA	GTG	TGT	GCT
429	M	V	L	T	T	L	I	L	I	L	V	C	A
1248	GAT	GTA	GCG	CTG	GCT	GCA	GTT	CTT	GTC	CCT	GTG	CTG	GTC
416	D	V	A	L	A	A	V	L	V	P	V	L	V
1209	GAT	ATC	AGA	AAT	ACT	ACC	GTA	ACT	CCA	AAT	GTA	ACC	AAA
403	D	I	R	N	T	T	V	T	P	N	V	T	K
1170	GAA	TTT	CCT	GCA	CAG	ACA	GAA	CAA	ACA	ACT	GCC	AGT	CCT
390	E	F	P	A	Q	T	E	Q	T	T	A	S	P
1131	CCA	AAA	TTT	ACG	CAA	CCA	CTA	CAA	CCT	CGC	AGT	AGC	AAT
377	P	K	F	T	Q	P	L	Q	P	R	S	S	N
1092	AAC	ACT	ACA	GCC	CCT	CCA	AAA	ATA	GCC	AAA	GGT	CGT	GCC
364	N	T	T	A	P	P	K	I	A	K	G	R	A
1053	ACT	CAA	CCT	CCA	CCT	CCT	CGG	AAC	AGC	AAT	GAC	CTC	AAA
351	T	Q	P	P	P	P	R	N	S	N	D	L	K

FIG. 4

1599	GAA	GGA	AAA	GAA	GCA	GGC	TAT	GCA	GAC	CTA	GAT	CCT	TAC
546	N	S	P	G	Q	E	V	Y	H	A	Y	A	E
1638	AAC	TCA	CCA	GGG	CAG	GAA	GTT	TAT	CAT	GCC	TAT	GCT	GAA
559	P	L	P	I	T	G	P	E	Y	A	T	P	I
1677	CCA	CTC	CCA	ATT	ACG	GGG	CCT	GAG	TAT	GCA	ACC	CCA	ATC
572	I	M	D	M	S	G	H	P	T	T	S	V	G
1716	ATC	ATG	GAC	ATG	TCA	GGG	CAC	CCC	ACA	ACT	TCA	GTT	GGT
585	Q	P	S	T	S	T	F	K	A	T	G	N	Q
1755	CAG	CCC	TCC	ACA	TCC	ACT	TTC	AAG	GCT	ACG	GGG	AAC	CAA
598	P	P	P	L	V	G	T	Y	N	T	L	L	S
1794	CCT	CCC	CCA	CTA	GTG	GGA	ACT	TAC	AAT	ACA	CTT	CTC	TCC
611	R	T	D	S	C	S	S	A	Q	A	Q	Y	D
1833	AGG	ACT	GAC	AGC	TGC	TCC	TCA	GCC	CAG	GCC	CAG	TAT	GAT
624	T	P	K	A	G	K	P	G	L	P	A	P	D
1872	ACC	CCG	AAA	GCT	GGG	AAG	CCA	GGT	CTA	CCT	GCC	CCA	GAC
637	E	L	V	Y	Q	V	P	Q	S	T	Q	E	V
1911	GAA	TTG	GTG	TAC	CAG	GTG	CCA	CAG	AGC	ACA	CAA	GAA	GTA
650	S	G	A	G	R	D	G	E	C	D	V	F	K
1950	TCA	GGA	GCA	GGA	AGG	GAT	GGG	GAA	TGT	GAT	GTT	TTT	AAA
654	E	I	L	*									
1962	GAA	ATC	CTT	TGA									

Tissue Expression profile of LCP

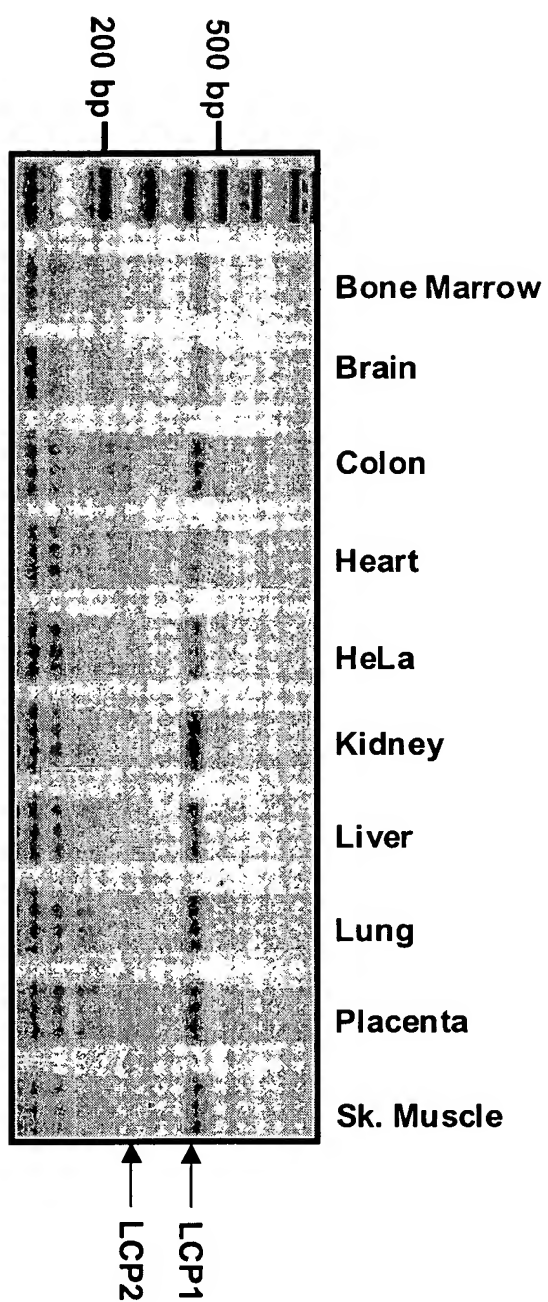


FIG. 5